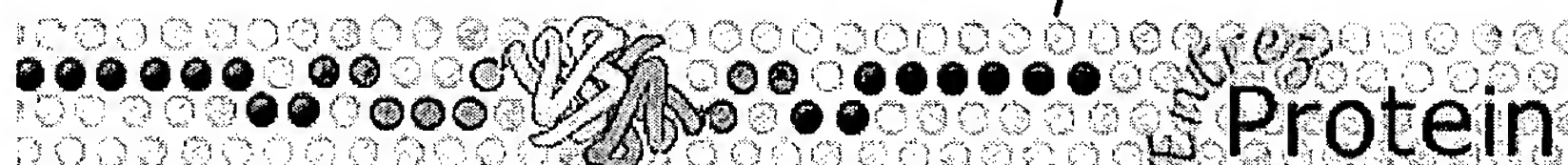


Appendix A

APPLICANTS
COPY

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search Protein for Go Clear

Limits Preview/Index History Clipboard Details
Display default Show: 20 Send to File Get Subsequence Feat☐ 1: Q15012. Lysosomal-associa...[gi:3122413] BLink, Domains, Links

LOCUS Q15012 233 aa linear PRI 15-MAR-2004

DEFINITION Lysosomal-associated transmembrane protein 4A (Golgi
4-transmembrane spanning transporter MTP).

ACCESSION Q15012

VERSION Q15012 GI:3122413

DBSOURCE swissprot: locus MTRP_HUMAN, accession Q15012;

class: standard.

created: Jul 15, 1998.

sequence updated: Jul 15, 1998.

annotation updated: Mar 15, 2004.

xrefs: gi: 285962, gi: 40788948, gi: 33875421, gi: 12653305

xrefs (non-sequence databases): GenewHGNC:6924, InterProIPR004687,
PfamPF03821, TIGRFAMsTIGR00799

KEYWORDS Transmembrane; Transport.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 233)

AUTHORS Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S.,
Tabata,S., Ishikawa,K.-I., Kawarabayasi,Y., Kotani,H. and Nomura,N.

TITLE Prediction of the coding sequences of unidentified human genes.

III. The coding sequences of 40 new genes (KIAA0081-KIAA0120)

deduced by analysis of cDNA clones from human cell line KG-1

JOURNAL DNA Res. 2 (1), 37-43 (1995)

MEDLINE 95308325

PUBMED 7788527

REMARK SEQUENCE FROM N.A.

TISSUE=Bone marrow

REFERENCE 2 (residues 1 to 233)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REMARK SEQUENCE FROM N.A.
TISSUE=Muscle

COMMENT -----
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[FUNCTION] May function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment (By similarity).
[SUBCELLULAR LOCATION] Integral membrane protein. May reside in an intracellular membrane-bound compartment (Potential).
[DOMAIN] The C-terminal domain is necessary for retention within intracellular membranes (By similarity).

FEATURES

	Location/Qualifiers
source	1..233 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..233 /gene="LAPTM4A" /note="synonyms: MTRP, KIAA0108"
Protein	1..233 /gene="LAPTM4A" /product="Lysosomal-associated transmembrane protein 4A"
Region	29..49 /gene="LAPTM4A" /region_name="Transmembrane region" /note="Potential."
Region	82..102 /gene="LAPTM4A" /region_name="Transmembrane region" /note="Potential."
Region	108..128 /gene="LAPTM4A" /region_name="Transmembrane region" /note="Potential."
Region	160..180 /gene="LAPTM4A" /region_name="Transmembrane region" /note="Potential."
Region	226..229 /gene="LAPTM4A" /region_name="Domain" /note="Poly-Pro."

ORIGIN

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121 vlscslvaiss ltylprikey ldqlpdfpyk ddllaldssc llfivlvffa lfiifkayli
181 ncvwnckykyi nrrnvpeiav ypafeappgy vlptyemavk mpekeppppy lpa
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